

Concordance of Cranial and Dental Morphological Traits and Evidence for Endogamy in Ancient Egypt

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ABSTRACT A biological affinities study based on frequencies of cranial nonmetric traits in skeletal samples from three cemeteries at predynastic Naqada, Egypt, confirms the results of a recent nonmetric dental morphological analysis. Both cranial and dental traits analyses indicate that the individuals buried in a cemetery characterized archaeologically as high status are significantly different from individuals buried in two other, apparently non-elite cemeteries and that the nonelite samples are not significantly different from each other. A comparison with neighbouring Nile Valley skeletal samples suggests that the high status cemetery represents an endogamous ruling or elite segment of the local population at Naqada, which is more closely related to populations in northern Nubia than to neighbouring populations in southern Egypt. © 1996 Wiley-Liss, Inc.

The origins of the ancient Egyptian state may be traced to the rapid social and political changes that occurred in Upper (southern Egypt during the predynastic period (approximately 5000 to 3050 BC) and which ended with the unification of Upper and Lower Egypt in the first of thirty ruling dynasties (Bard, 1994a,b). Early attempts to explain this phenomenon were not sympathetic to the possibility that Egyptian civilization could have developed from indigenous origins, however, and instead postulated its origin in the immigration of foreigners from southwest Asia or the circum-Mediterranean (e.g., Derry, 1956; Emery, 1967; Petrie, 1920, 1939). In the following decades a number of studies have investigated the biological relationships among temporally and spatially diverse Nile Valley populations (e.g., Berry and Berry, 1972; Berry et al., 1967; Brace et al., 1993; Greene, 1982; Johnson and Lovell, 1994; Keita 1990, 1992; Pääbo and Di Rienzo, 1993; Prowse and Lovell, 1995; Rösing, 1989, 1990; Strouhal, 1968, 1971), but the question of population affinities

during the formation of the Egyptian state has yet to be conclusively resolved.

To investigate the biological associations of Egyptian state formation we have examined the population affinities of the earliest socially stratified groups, which appear unarguably during the predynastic period at the site of Naqada. Naqada had an important role as a religious and political center at this time, and its functions would have required an administrative or managerial elite (Bard, 1994a,b; Hassan, 1988; Trigger, 1983). The apparent presence of palatial houses in a settlement area (Hassan, 1988) and the existence of a cemetery for an elite segment of the population, such as chieftains (Case and Payne, 1962) or kings (Kemp, 1973), provide material evidence in this regard, although whether this social differentiation is the result of cultural differences (e.g.,

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the accumulation of wealth) or biological differences (e.g., the immigration of foreigners) has not been firmly established. The answer to this question is important because the social stratification documented at Naqada is considered by many to be the precursor of the highly visible and well-established social inequality that is characteristic of the later dynastic periods and which is manifested, for example, in monumental architecture such as the pyramids of Giza (approximately 2589 to 2504 BC) and in mortuary opulence for those of high status, such as King Tutankhamun (approximately 1334 to 1325 BC).

The Naqada cemeteries were excavated by Petrie in 1894–1895: Cemetery T (named for its location near two tumuli), Cemetery B (named after the nearby mound called Kom Bellal), and the Great Cemetery (named for the “Great New Race” that was mistakenly identified by Petrie when he discovered previously unknown cultural remains). Cemetery T is generally agreed to be the burial place of an elite segment of the population because of its small, localized area, the richness of its grave goods (Bard, 1989, 1992; Castillos, 1981; Davis, 1983; Petrie and Quibell, 1896), and the patterning of different types of grave goods (Fekri Hassan, personal communication).

A recent analysis of nonmetric dental morphological trait variation has shown that individuals buried in the elite cemetery at Naqada are biologically differentiated from those buried in the two nonelite cemeteries, which are not significantly different from each other (Johnson and Lovell, 1994). In this paper we present the results of an analysis of cranial nonmetric trait variation among the same three cemetery samples and among skeletal samples from neighbouring regions of Upper Egypt and Lower Nubia. This study thus addresses the question of whether cranial and dental nonmetric traits analyses lead to the same results and also provides an independent line of evidence in the investigation of biological relationships during the development of social complexity in ancient Egypt.

MATERIALS AND METHODS

Early research in comparative anatomy and physiology, embracing the concept of re-

capitulation, identified skeletal nonmetric traits as anomalies that were evolutionary vestiges of features seen in lower mammals (Blumenbach, 1776; Henle, 1855; Hyrtl, 1859; Krause, 1880; LeDouble, 1903; Oettinger, 1930; Quain, 1908; Sullivan, 1922; Testut, 1889) and thus compared human populations on the premise that ancestral traits were evidence of racial primitiveness (Morton, 1839; Scott, 1893). When the theory of recapitulation was rejected, attention turned to metric studies of variation, but nonmetric trait analysis regained credence when a model was proposed for the genetic control of trait inheritance in mice (Grüneberg, 1952). This model provided a theoretical justification for the study of morphologically analogous traits in humans and led to familial studies of the inheritance of skeletal variants (Cheverud and Buikstra, 1981a,b, 1982; Johnson et al., 1965; Pietrusewsky and Douglas, 1993; Saunders and Popovich, 1978; Saunders et al., 1976; Suzuki and Sakai, 1960; Torgersen, 1951a,b). Subsequently, indirect evidence for the genetic basis of some traits in humans was obtained from studies of wild and laboratory populations of mice (*Mus musculus*) (Berry, 1963, 1964; Grewal, 1962; Grüneberg, 1951, 1952, 1955; Howe and Parsons, 1967; Searle, 1954a,b), while direct evidence was obtained from traits that appear before birth (El-Najjar and Dawson, 1977) and from agreements in trait frequencies among related groups (Pietrusewsky and Douglas, 1993).

The relative ability of metric and nonmetric traits to determine human biological affinities was the subject of much debate during the 1970s and 1980s. Berry and Berry's oft-cited study (1967) contended that nonmetric traits were superior to metric traits because of the apparent lack of correlations with age and sex and between individual traits, minimal influence of environmental factors, and relative ease of scoring, but numerous subsequent studies were unable to reach a consensus on the relative merits of nonmetric vs. metric traits when evaluated in the light of linguistic or cultural data (Carpenter, 1976; Ossenberrg, 1977; Rightmire, 1972; Sjøvold, 1977; Thoma, 1981). The controversy appeared to be resolved when it was demonstrated that both types of traits

shared similar developmental patterns and were, therefore, alternative expressions of the same underlying continuous variable (Cheverud et al., 1979; Corruccini, 1976). Significant age, sex, and intertrait correlations were reported (Corruccini, 1974), however, generating extensive research on the methodological aspects of nonmetric trait analysis. Previously held assumptions concerning the negligible effects of age and sex on nonmetric trait frequencies, for example, have been found to be invalid, and therefore trait frequencies must be examined for possible age and sex associations prior to further analysis. Although the genetic basis for the inheritance of some nonmetric traits in humans has been accepted now by most researchers the selection of traits must be made with reference to the etiology and development of traits (Hauser and De Stefano, 1989; Rösing, 1984).

The samples used in this study reflect the consideration of both space and class in our formulation of the problem and consist of crania from the two nonelite cemeteries, Cemetery B ($n = 35$) and the Great Cemetery ($n = 63$), and from the elite cemetery, T ($n = 37$), at predynastic Naqada and from neighbouring predynastic Badari ($n = 57$), Qena ($n = 37$), and protodynastic Lower Nubian Site 277 ($n = 35$) (Fig. 1). The dates for these sites were first based on Petrie's relative Sequence Dates (Petrie, 1901) as the Amratian, Gerzean, and Semainean periods which were later revised and called the Naqada I, II, and III periods (Kaiser, 1956, 1957). The Badarian cultural period long has been thought to slightly predate Naqada I. There are few radiocarbon dates for these time periods even though Libby's (1955) early application of the technique produced dates (albeit apparently erroneously old) for a number of ancient Egyptian sites (for a review see Hassan, 1988). Badari is the earliest of the sites we have sampled; recent work indicates that the Badarian cultural period in the region of Badari itself likely is coeval with Naqada I and dates to approximately 3800 BC (Holmes and Friedman, 1989). The three Naqada cemeteries appear to have been used contemporaneously during Naqada II and III, dating to approximately 3600 to 3000 BC (Bard 1989; Hassan

1988), while the cemetery at Qena was used during late Naqada II and Naqada III (approximately 3400 to 3000 BC).¹ The Lower Nubian site is the most recent in our study, dating to the terminal A-Group period of Lower Nubian culture, approximately 3000 to 2750 BC (Vagn Nielsen, 1970). The total time frame that we have sampled, then, is in the neighbourhood of 800 years. Although a temporal approach to the problem of biological affinities at Naqada (i.e., comparing Naqada I, II, and III samples from the same cemetery or site) might prove profitable, the precision of dates, their attribution to specific graves, and the size of the available samples, unfortunately, are inadequate for such a study.

Fifty-eight nonmetric traits were selected for study, on the basis of whether published sources revealed a good understanding of their development, demonstrated their predominantly genetic control, and provided data suitable for an extended comparative study (Berry et al., 1967; Brothwell, 1972; Buikstra, 1976; Hauser and DeStefano, 1989; Ossenberrg, 1970; Rose et al., 1991). Bilateral traits were scored using the side count method, and partial trait manifestations were scored as present. All data were collected with reference to standardized scoring procedures (including both trait descriptions and illustrations from the original sources) since this reduces intra- and inter-observer error to acceptable levels (Molto, 1979). Only traits that were observed in at least two samples were included in the analysis since the influence of chance occurrences of rare traits can be magnified if traits that appear in only one of the samples are included. Traits that were completely absent or that had 100% frequency in all samples also were eliminated, reducing the final data set to 47 traits (Table 1).

Since the crania were not curated with their postcranial skeletons, we used standard morphological features of the cranium to determine sex (Bass, 1987; Brothwell,

¹Excavation reports for Qena have never been published, but Lovell examined the excavator's original field notes, which are archived at the Museum of Fine Arts, Boston, and which attribute the cemetery to the late Naqada II and Naqada III periods.

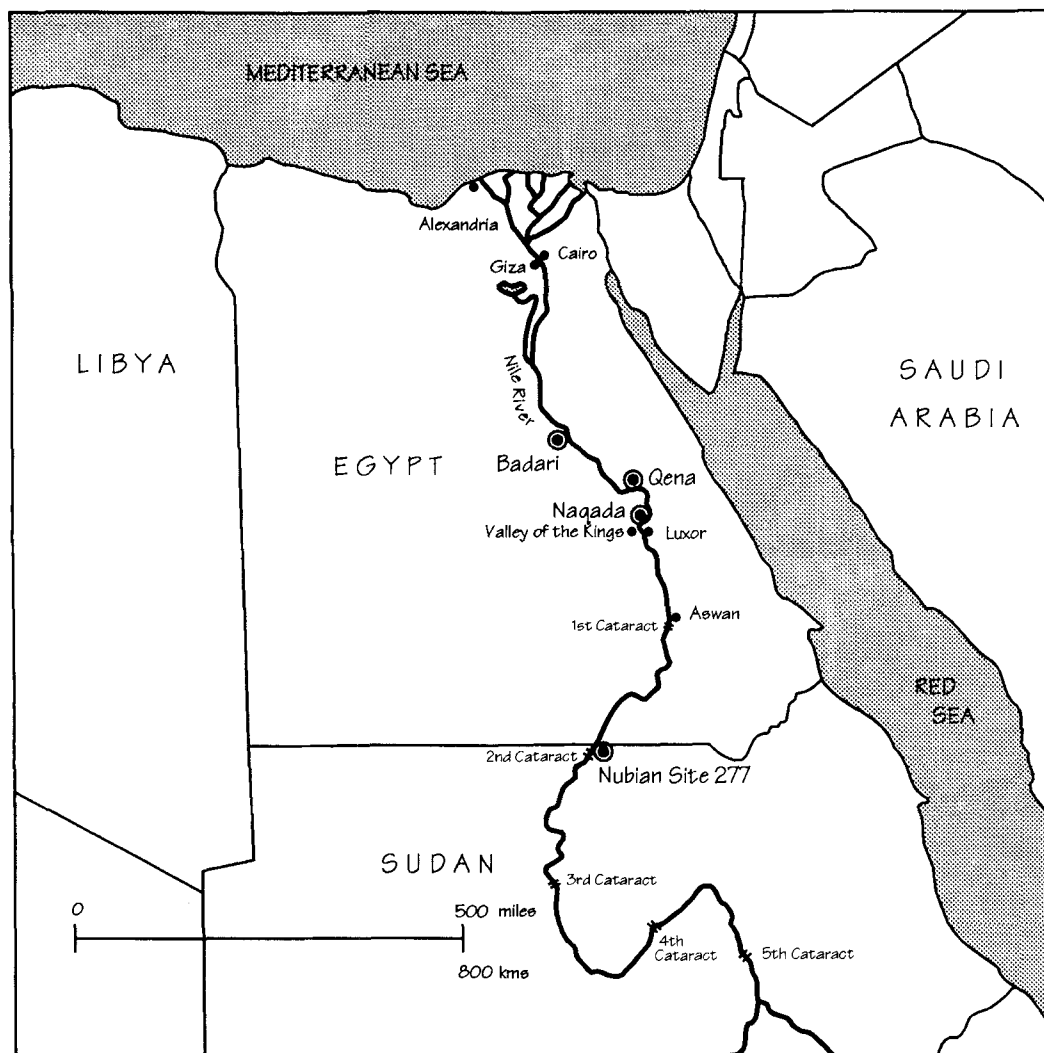


Fig. 1. Map of modern Egypt and Sudan showing the locations of the predynastic sites of Naqada, Badari, and Qena and the protodynastic Nubian Site 277.

1972; Ubelaker, 1989; White, 1991) and degree of ectocranial suture closure to estimate age at death (Meindl and Lovejoy, 1985). To facilitate data analysis, individuals were categorized as subadult (≤ 20 years), young adult (21–30 years), middle adult (31–40 years), or older adult (> 40 years). Extremely fragmentary crania were assigned to these age groups after being seriated on the basis of relative degrees of molar wear, with wear standards having been estimated from those crania of “known” age in the sample. Only

adult crania were included in this study because the development of many traits is age-progressive (Berry et al., 1967; Buikstra, 1976; Perizonius, 1979). Age and sex correlations with nonmetric trait frequencies were tested and, since there were no significant associations, ages and sexes were pooled for further analysis. Although intertrait correlations are considered by some workers to affect the outcome of biological affinities analysis, they were not viewed as a factor in this study since previous research has found

TABLE 1. Frequencies of cranial nonmetric traits for the Naqada cemeteries, ages and sexes pooled

Traits	Cemetery B		Cemetery T		Great cemetery	
	n ¹	N ²	n ¹	N ²	n ¹	N ²
Highest nuchal line	6	50	4	58	2	108
Ossicle at lambda	4	22	4	29	5	52
Inca bone	1	24	2	29	0	52
Lambdoidal suture ossicle	10	34	13	49	24	73
Biasterionic suture ³	3	38	7	48	4	101
Ossicle at asterion ³	8	39	3	53	10	105
Parietal foramen ³	32	50	42	60	63	106
Obelionic foramen	0	26	3	30	2	50
Coronal suture ossicle	1	30	2	43	4	78
Sagittal suture ossicle	2	15	1	15	4	34
Epipteric bone ³	2	27	6	40	12	92
Parietal notch bone ³	3	41	4	53	8	102
Parietal notch present ³	22	42	39	53	92	102
Occipitomastoid wormians ³	5	36	2	45	3	95
Sutural foramen ³	23	42	24	46	59	94
Mastoid foramen ³	33	42	31	46	71	94
Occipital foramen ³	6	42	4	46	9	94
Tympanic dehiscence ³	4	53	13	46	10	101
Posterior condylar canal patent ³	13	34	12	34	20	79
Condylar facet double ³	0	40	1	35	2	90
Precondylar tubercle	15	44	19	38	22	94
Paracondylar process ³	15	26	10	32	44	82
Anterior condylar canal double ³	14	45	11	43	30	96
Foramen ovale incomplete ³	2	31	3	45	6	92
Foramen spinosum open ³	10	31	13	45	33	91
Pterygo-alar spurs ³	0	5	1	7	3	25
Accessory lesser palatine foramen ³	17	33	17	23	58	79
Palatine torus	1	18	6	14	6	44
Zygomaxillary tubercle ³	27	30	26	32	76	89
Marginal tubercle ³	25	32	36	36	82	88
Zygomatico-facial foramen ³	25	29	30	34	66	88
Supraorbital foramen ³	25	44	29	57	48	106
Accessory supraorbital foramen ³	4	44	4	56	7	106
Metopism	0	23	1	29	2	53
Frontal foramen/notch ³	4	44	13	57	19	106
Frontal grooves ³	6	45	18	54	29	106
Posterior ethmoid foramen ³	6	8	24	25	49	54
Nasal bone sutures	0	17	4	18	3	39
Accessory infraorbital foramen ³	4	28	3	29	8	84
Infraorbital suture ³	12	24	19	29	53	86
Accessory mental foramen ³	3	29	1	24	4	84
Rocker jaw	2	10	5	11	11	35
Mylohyoid arch ³	2	22	4	24	5	79
Lingula bridge ³	0	25	2	24	5	79
Genial tubercles	12	15	10	13	38	43
Median mental spine	8	15	5	13	30	43
Genial pits	9	15	11	12	29	43

¹ n = number of sides where the trait is present.² N = total number of observable sides.³ Bilateral trait frequencies are based on right plus left sides.

that correlations between traits in small samples such as these are rarely statistically significant (Berry et al., 1967; Corruccini, 1974; Saunders, 1978, 1989; Sjøvold, 1973, 1977).

Because of these small sample sizes, trait frequencies were arcsine-transformed before analysis using the Freeman and Tukey transformation recommended by Green and Suchey (1976). Comparisons were then made among the three samples using the

multivariate Mean Measure of Divergence (MMD) statistic. The MMD value, its variance, and its standard deviation were calculated according to the mathematical models of Green and Suchey (1976) and Sjøvold (1973). A standardized MMD value is used in this study to measure the biological affinities of the samples since standardized scores should be used when comparing samples of different sizes (Hemphill et al., 1991; Sofaer et al., 1986). Standardized MMD values are

calculated by dividing each raw MMD score by its standard deviation. The MMD statistic is used for significance tests; it indicates similarity or dissimilarity rather than the degree of relatedness of populations. A standardized MMD value greater than 2.0 is considered statistically significant at the 0.05 probability level (Sjøvold, 1973). The standardized MMDs were then subjected to cluster analysis using Ward's method (Ward, 1963), which is a hierarchical agglomerative statistic based on the minimum distance of the items in a cluster from the mean of that cluster.

RESULTS

The frequencies of the cranial nonmetric traits in the six cemetery samples, ages and sexes pooled, are presented in Table 1. Table 2 gives the raw MMD scores, standard deviations, and the corresponding standardized MMDs for the Naqada samples, which indicate that Cemetery B and the Great Cemetery are not statistically distinguishable from each other but that Cemetery T is significantly different from both Cemetery B and the Great Cemetery. Table 3 presents the MMD data for Badari, Qena, and Nubia in addition to Naqada and shows that these samples are all significantly different from each other. Since the two nonelite samples from Naqada are not significantly different, they were pooled for the cluster analysis that is presented in Figure 2 and which demonstrates that 1) the Naqada samples are more similar to each other than they are to the samples from the neighbouring Upper Egyptian or Lower Nubian sites and 2) the Naqada samples are more similar to the Lower Nubian protodynastic sample than they are to the geographically more proximate Egyptian samples.

The MMD is a test of significance and as such measures similarity without necessarily demonstrating relationship. Since the nonmetric traits used in this study are under genetic control, however, it is reasonable to interpret this result as indicating biological relatedness, at least in the case of the two nonelite samples from Naqada, which we have pooled. Further, although the elite and nonelite samples from Naqada are biologi-

TABLE 2. Results of the test of biological affinity among two nonelite cemeteries (B and Great) and one elite cemetery (T) at Naqada using the mean measure of divergence (MMD) statistic

	Cemetery comparison		
	B-Great	B-T	T-Great
MMD	0.018	0.054	0.025
Standard deviation of MMD	0.013	0.019	0.012
Standardized MMD ¹	1.363	2.847 ²	2.033 ²

¹ Standardized MMD = MMD/Standard Deviation of MMD.

² Statistically significant differences.

cally different on the basis of the MMD statistic, the fact that cluster analysis places them closest to each other in the dendrogram (Fig. 2) suggests a closer biological affinity to each other than to the other skeletal samples analyzed.

DISCUSSION AND CONCLUSIONS

The results of this analysis of cranial nonmetric trait variation indicate that the individuals buried in Cemetery T can be differentiated from those buried in the other two, nonelite cemeteries at Naqada. Further, the skeletal populations of the two nonelite cemeteries derive from a biologically homogeneous group. These results support those obtained for nonmetric dental morphological traits on the same samples (Johnson and Lovell, 1994). Although the small number of dental traits available for examination may have affected the reliability of the earlier study, the work reported here corroborates those findings using an independent line of evidence based on a much larger sample.

The observed biological differentiation cannot be attributed to chronological variation among the Naqada cemeteries since recent reassessments of their dating indicate that they were used contemporaneously during the middle and late Naqada cultural periods (Bard, 1989, 1994a; Davis, 1983). The distinction also cannot be attributed to in situ evolution between these middle and late cultural sequences, a period of only 600 years. Although mutations serve to increase variation among populations separated by time, mutation rates are much lower (approximately 1×10^{-6} [Cummings, 1988]) than what would be needed to support the size of the observed distinction.

Alternatively, the distinction of Cemetery

TABLE 3. Matrix of standardized mean measures of divergence (MMD) and their standard deviations¹

Skeletal samples	Badari	Qena	Naqada Great and B	Naqada T	Nubia
Badari	—	0.001	0.00	0.00	0.00
Qena	13.19	—	0.001	0.001	0.001
Naqada Great & B	17.69	17.70	—	0.00	0.00
Naqada T	8.22	12.83	2.57	—	0.00
Nubia	12.85	7.61	8.49	5.17	—

¹All Standardized MMD values are statistically significant. Standardized MMDs are in bold on the lower left side of the table; standard deviations are on the upper right side.

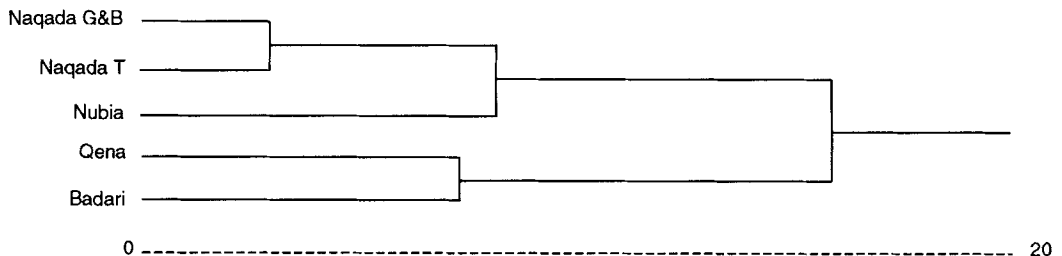


Fig. 2. Dendrogram showing the relationships of five pre- and protodynastic Nile Valley skeletal samples, based on Ward's method (Ward, 1963). The scale represents the cumulative error sum of squares associated with successive linkages in the cluster analysis of the matrix presented in Table 3.

T could reflect the presence of an immigrant elite population at Naqada, although the consistency of style (if not richness) of grave goods among the cemeteries argues against this. Further, people undoubtedly travelled along the Nile River, but there is no archaeological evidence for large population movements; rather, subsistence or trade activities by individuals or families probably characterize travel at this time. This does not rule out some gene flow, but we believe that the magnitude of the differences can be most parsimoniously explained by other processes whereby Cemetery T represents an elite segment of the population that became biologically differentiated from the rest of the community's inhabitants either through genetic drift, or through positive assortative mating (inbreeding) within the social group. The high frequency of a rare trait (palatine torus) in the Cemetery T sample as compared to the other samples may be indicative of kin relationships, as has been demonstrated, for example, for an Old Kingdom sample at Aswan (Rösing, 1982, 1986, 1990). Within-group marriage is well documented for the Egyptian nobility in later times.

Overall, our results suggest that there was a significant degree of biological heterogeneity among Nile Valley populations during the early periods of Upper Egyptian and Lower Nubian cultural history, as has been demonstrated previously by craniometric analyses (Keita, 1992) and which fits with a variety of historical, cultural, and linguistic data (reviewed by Keita, 1993). This heterogeneity, however, likely reflects normal variability among human populations. It has been hypothesized that periods of severe aridity in the Sahara prior to the Egyptian predynastic forced people to move into the Nile valley and come into contact with indigenous Nilotic groups (Hassan, 1988), and thus the source of the observed variability in predynastic populations may be the presence and interaction of numerous biologically distinct groups within the Nile Valley (Keita, 1992). The Naqada-Lower Nubia cluster is consistent with the archaeological evidence for trade relations between Upper Egypt and Nubia at this time (Smith, 1991; Trigger, 1983), and the results of our study suggest that these cultural associations may reflect biological affinities. While the relationships

among populations of Upper Egypt, Lower Egypt, and Palestine, for which there exists archaeological evidence for contact, also should be examined, the high water table in the Egyptian delta has led to very poor preservation of skeletal remains which has hindered such analysis.

Although it cannot be determined conclusively from our results whether the higher status of the Cemetery T individuals derives from an accumulation of material wealth or from a religiopolitically determined "royal" heritage, the conditions favoring genetic drift are such that status at Naqada was likely ascribed rather than achieved. Thus, the origins of the Egyptian state may very well lie in a sociopolitical organization that was headed by ruling families or lineages.

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